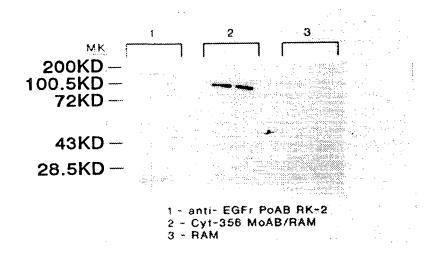
WO 94/09820

1813/424/277.1

1/48

FIGURE 1

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FIGURE 2A

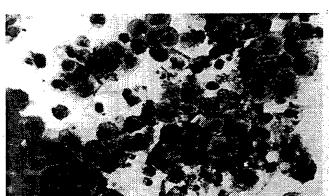


FIGURE 2B

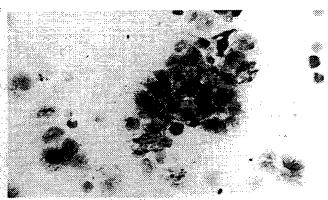


FIGURE 2C

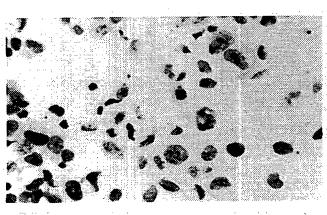


FIGURE 2D

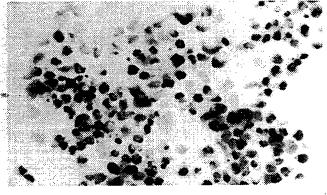


FIGURE 3A

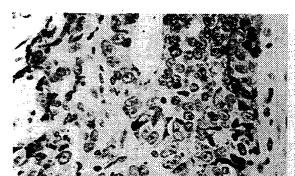


FIGURE 3B

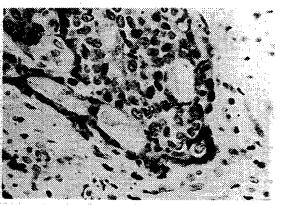


FIGURE 3C

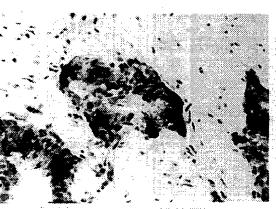
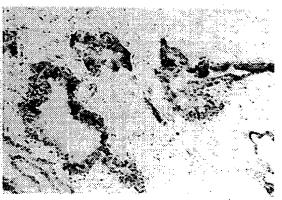


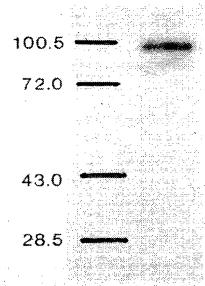
FIGURE 3D



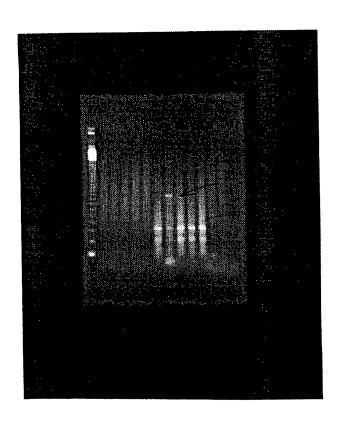
WO 94/09820 PCT/US93/10624

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FIGURE 4

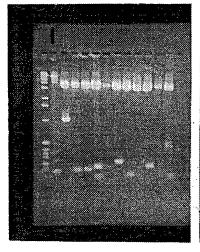


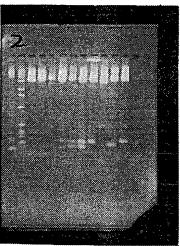
5/48 FIGURE 5



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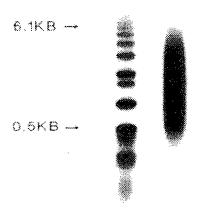
FIGURE 6A FIGURE 6B





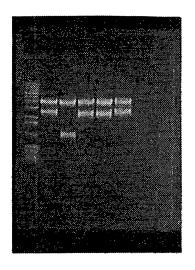
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FIGURE 7

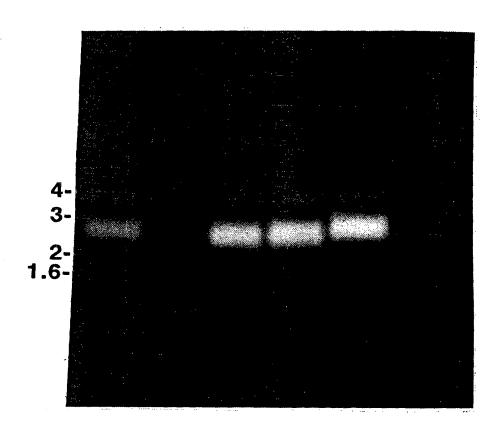


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FIGURE 8

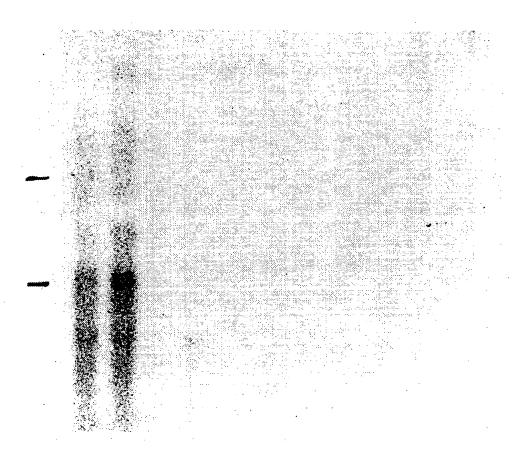


9/48 FIGURE 9



PCT/US93/10624

10/48 FIGURE 10



11/48 FIGURE 11

1 2 3
9.5___
7.5__

4.4__

2.4__

1.4__

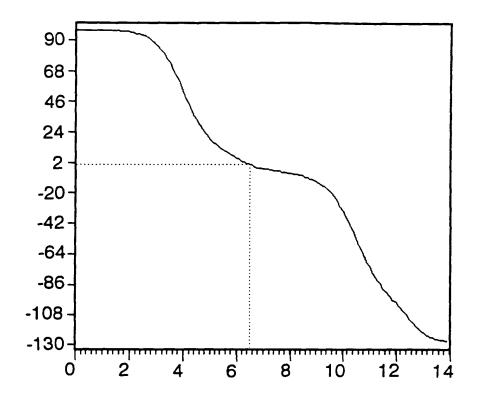
12/48

FIGURE 12A

FIGURE 12B

PCT/US93/10624

13/48 FIGURE 13



Done on sequence PMSANTIGEN. Total number of residues is: 750. Analysis done on the complete sequence

41.2% 2% . 4% 35. Â Â î î AA AA AA 264 309 76 101 CNAT CNAT CNAT -75 -88 00 11 Ħ II 11 conformation conformation conformation conformation EEECO Extended Helical Turn Coil In

14/48

Sequence shown with conformation codes.

are given conformation ಹ in or more residues വ stretch of Consecutive overlined

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回	ပ	回	धि	旧	<u> </u>	回	 臼	F	ပ	回	回	1
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91	121	151	181	211	241	271	301	331	361	391	421	

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 Ξ 田田 H IH IH 回 田 田 C H H 旧 C 田 IH 旧田 田 |田 C H 旧 H 曰 田 IH 一日 田田 旧 IH H H 田田 H IH H 田 C 日日 H H H 田 H IH 田田 旧 C 日 IH H H H 田 团 日 旧田 H 田 H IH H 10 团 IH 田 日 IH IH H 田田 H 10 IH IH 团 田田 H H H IH 团 IO C 田 C IH 田田 田 IH H 10 田 C IH 田 C IH IH IH H IU C IH 曰 IH IH IH C IH H 囝 H H IH 田 田 H H 团 H H IH 田 回 田 C IH 团 田田 H H IH 臼 H 田 C IH H 闰 田 闰 二二 IH 旧 IH H IH |田 团 田 田 IH 旧 回 田 11 田 IH 田 回 IH 田 田 团 日日 旧 IH H 田 旧 H 田 16 田田 IH IH 回 12 田田 田 IH 臼 田田 旧田 团 H IH 工 **|**円 回 田 IH 团 旧田 |FI 田田 IH IH |**日** 田 团 IH 10 田田 田 IH IH IH H 回 IH 10 H 旧田 一日 IH IH H C H 10 H H C 田田 IH IH H C II 10 IH IH 回 IH 臼 IH IH C H IH 10 IE H IH H 闰 H C H IH 曰 IH C H 旧 IH IH H IH C 王 旧田 IE H IH IH H 田 IH 田 C 旧 IH H IH IH 田 旧日 IH 团 C 田田 团 IH IH 王 田 **|**E H 臼 IH 田 H IH IH H 田 旧 U 541 571 601 451 481 511 631 661 691 721

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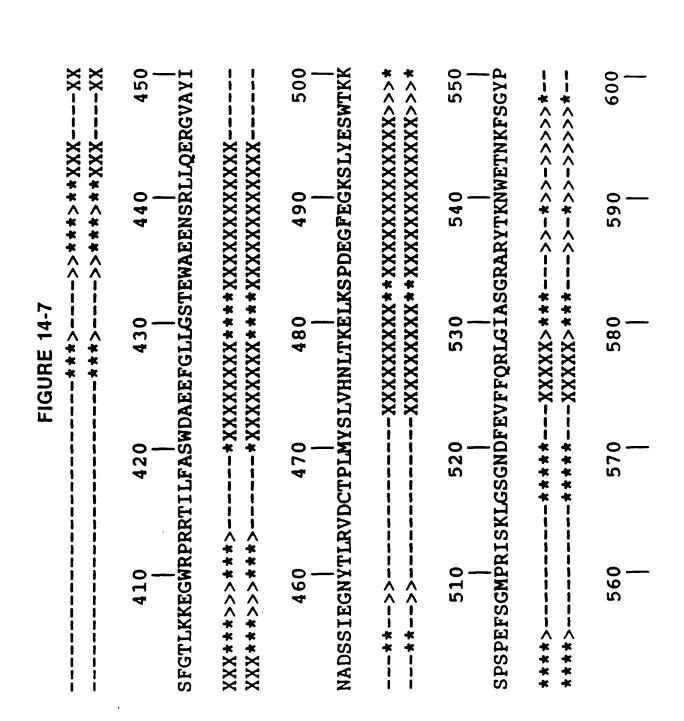
Extended conformation: conformation: 50 100 **MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEAT** X<*****XXXXXX----X<******XXXXXX--nitpkhnmkafldelkaenikkflynftqiphlagteqnfqlakqiqsqw Symbols used in the semi-graphical representation: 90 Coil FIGURE 14-4 30 80 ----<<---XXXXXXXXXXXXXXXX conformation: X ---<<---XXXXXXXXXXXXXXXX conformation: Semi-graphical output. 20 9 Helical Turn

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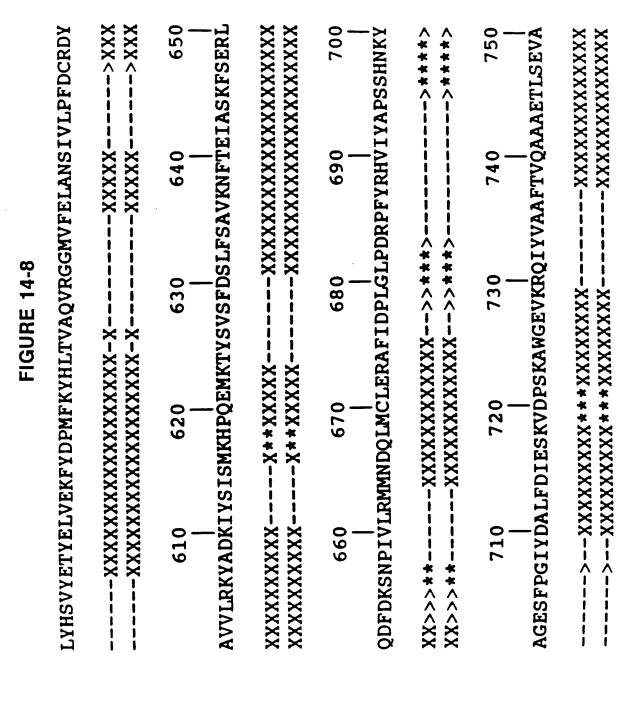
150 200 **KEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEPPPPG** ^^****^^----X**^*-----**^^^---^^****^^----X**^*-----**^^^-----XXXXXXX**^<--**YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKI** 140 190 130 180 170 120 --XXXXXXXX**< 110 160

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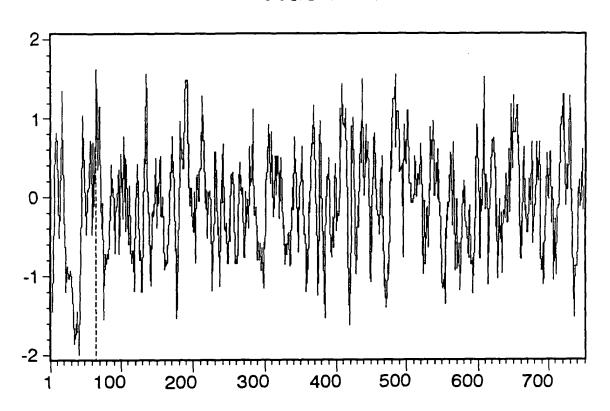
	250 WNLPG	**-\\\\	300 PIGYY		350 IHSTN	* * * * * * * * * * * * * * * * * * * *	400 HEIVR
-<< <xxxxxxxxxxxxxxxxxxxxx-< td=""><td>240 FAPGVKSYPDG</td><td>^</td><td>290 EAVGLPSIPVH</td><td> </td><td>340 GNFSTQKVKMH</td><td>XXXXXX*-*</td><td>390 GIDPQSGAAVV</td></xxxxxxxxxxxxxxxxxxxxx-<>	240 FAPGVKSYPDG	^	290 EAVGLPSIPVH	 	340 GNFSTQKVKMH	XXXXXX*-*	390 GIDPQSGAAVV
14-6	230 SVILYSDPADY		280 ANEYAYRRGIA	XX	330 KVPYNVGPGFT		380 LGGHRDSWVFG
FIGURE -**>***	220 VKNAQLAGAKO	->**XXXXXXX**<-	270 AGDPLTPGYPA	***	320 PPDSSWRGSLJ		370 GAVEPDRYVI
\	210 220 230 240 250 VIARYGKVFRGNKVKNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNLPG	* ^	260 270 280 290 300 GGVQRGNILNLNGAGDPLTPGYPANEYAYRGIAEAVGLPSIPVHPIGYY	*^^^	310 320 330 340 350 DAQKLLEKMGGSAPPDSSWRGSLKVPYNVGPGFTGNFSTQKVKMHIHSTN	XXXXXXX->>>+****>	360 370 380 390 400 EVTRIYNVIGTLRGAVEPDRYVILGGHRDSWVFGGIDPQSGAAVVHEIVR



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FIGURE 15B

Done on sequence PMSANTIGEN. Total number of residues is: 750. Analysis done on the complete sequence.

-> This is the value recommended by the authors The averaging group length is: 6 amino acids. The method used is that of Hopp and Woods.

The three highest points of hydrophilicity are:

Asp-Glu-Leu-Lys-Ala-Glu Asn-Glu-Asp-Gly-Asn-Glu 68 137 to to 132 From From 1.57 1.62

Lys-Ser-Pro-Asp-Glu-Gly 487 to 482 From 1.55

Ah stands for: Average hydrophilicity.

control proteins, only the highest point was in 100% and third point: a known antigenic group. The second of incorrect predictions Note that, on a group of of the cases assigned to proportion of 33% gave a

SUBSTITUTE SHEET (RULE 26)

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opt	321	311	266	321	. 	3, . .	-			
init1	120	164	145	120 33	GGTTA	GGCTT	40	AGTAT :: CACAT		:: GGAGA 1160
			145	203 1	1070 CACCA	CCCCA	1040	1130 TTCCA.:::	1190	AAAA1GGGTGG :::::::: AAAATGGATGG 1150
initn	7		cd 1	7	CTCTCA	:: :: CTTACA	1030	rtggtc ::: caggac		:::: :::: :::: ::::
	or	ıd.	ıplete	cor	1060 AGACC	TGGAACTGGAGACCCTTACACCCCAGG	Ä	.0 1120 1130 :TGCAGAGGCTGTTGGTCTTCC : :: :: :: :: :: :: :: :: :: :: :: :: :	1180	CCIAG : :GTTCA(
	receptor	3' er	A, com	recept	0 TGCAGG	AACTGG	1020	O TGCAGAG : :: AGTTGAA		CAGGCTG
FIGURE 16-1	errin	mRNA,	or mRN	errin	1050 GAATGGT	CCTTGG		3GCGTGGAATT::::-GTTTCCACCA	1170	STGCAGCAGAGCTC STGCAGCAGGCTG 1130
FIGUR	G.gallus mRNA for transferrin recepto	ceptor	transferrin receptor mRNA, complete	for transferrin receptor nt overlap	1020 1030 1040 1050 1060 1070 TGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACCAGGTTA	CGGACATGCCCACCTTGGAACTGGAGACCCTTACACCCCAGGCTT	1010	1080 1090 1100 1110 1120 1130 CCCAGCAAATGAATAGCCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAAGTAT :::::::::::::::::::::::::::::::::	1160	TCCTGTTCATCCAATTGGATGCACAGAAGCTCCTAGAAAAATGGGTGGCTC TGCTGTTCAGACCATCTCTAGCAGTGCAGCCAGGCTGTTCAGCAAAATGGATGG
	A for	cin re	errin		1 PATCCT	GGACA	00	ICCTTAGE		CTCTAG
are:	S mRNA	nsfer	ransfe	G.gallus mRNA identity in 717	1030 'GGAAAT	CCATT	100	1090 GAATATG : :	1150	SACCATO
scores a	.gallu	at tra	Human t	gallu. ntity	CAGCGT	CTTATC	066	O AGCAAAT : TTCGTTC		CTGTTCAG CTGTTCAG
						TACAC	O,			
The best	CHKTFER	RATTRFR	HUMTFRR	CHKTFER 51.9%	pmsgen	CHKTFE TACACTTATCCCATT		pmsgen CHKTFE		pmsgen CHKTFE
	SUBSTITUTE SHEET (RULE 26)									

corge	: CAA 1210	Saagt ::: aaaga	FATGT ::::: FATGT	GGAGC ::::
1250 TGTTGGA	:: :: GGTGA(1310 TACCAATC : ::: TTCCATGA	1370 AGACAGA7 :: : : FGATCGG7	1430 FCAGAGTGGAG : ::: FGGCACTGGAA 1380
1240 rgccctacaa	::: ::: :::TTCCTGTAAGGTGACAA 1200 1200	1300 ACATCCACTC : :: ATGTGAACAA	1360 1370 AGTGGAACCAGACAGATATG : ::::: TGAAGAACCTGATCGGTATG	1420 TATTGACCCTCA : : :: GGCTAAAGCTGG 1370
1230 AGTCTCAAAG	::: GATCCA 1190	1290 TCAAGATGCA : : : : : TGAAACTAGA	1340 1350 ATAGGTACTCTCAGAGGAGC : :: :: :: :: :: :: :: :: :: :: :: :: :	1410 rcrrrccrcc :: : scccAGGAGT
1200 1210 1220 1230 1240 1250 AGCACCACCAGATAGCAGCTGGAGAGGTCTCAAAGTGCCCTACAATGTTGGACCTGG	CACATGCTCTGA-AG-GTTGGAAAGGTGCGATCCA-	1260 1270 1280 1290 1300 1310 CTTTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACTCCACTCTACCAATGAAGT : ::::::::::::::::::::::::::::::::::	1320 1330 1340 1350 1360 1370 GACAAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAGA	1380 1390 1400 1410 1420 1430 CATTCTGGGAGGTCACCGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGC : :::: ::: ::: ::: :::: :::::::::::::
1210 CCAGATAGCAG	::::: CTCTGA-AGG 1170	1270 ::::::::::::::::::::::::::::::::::::	1330 ATTTACAATGT ::::::::	1390 GGAGGTCACCGG :::: :: : GGAGCCCAGAGA
			1320 GACAAGAA : : : CAGGAAGA	1380 139 CATTCTGGGAGGT : :::: TGTGATTGGAGCC 1330
pmsgen	CHKTFE	DIMS DE CHIKE TEE CHIKE TEE (RU	pmsgen CHKTFE	pmsgen CHKTFE

	26/	48	
1440 1460 1470 1480 1490 AGCTGTTGTTGAAATTGTGAGGAGCTTTGGAACACTGAAAAGGAAGGGTGGAG ::::::::::::::::::::::::::::::::::::	1500 1510 1520 1530 1540 1550 ACCTAGAAGAATTTTGTTTTGCAAGCTGGGATGCAGAAGAATTTTGGTTTC :::::::::::::::::::::::::::::	1560 1570 1580 1590 1600 1610 TACTGAGTGGGCAGAGATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATTAA :::::::::::::::::::::::::::::::	
1480 ACTGAAAAAGG : ::::::	1540 AGAATTTGGTC ::: ::: AGACTACGGAC 1490	1600 GCGTGGCGTGC : : CAAAGCTTTCA	1660 GTTGATTGTACA :: : :
1470 1480 1499 GAGCTTTGGAACACTGAAAAAGGAAGGGTG :::::::::::::::::::::::	1530 GGGATGCAGA :::::: GGAGTGCAGG	1590 TCCTTCAAGA : :: :: : TGCTGCATGC	1640 1650 GGAAACTA-CACTCTGAGA(::::::::::::::::::::::::::::::::::::
1460 FGTGAGGA :: ::::	1520 STTTGCAAGCT X::::::::	1580	1640 AAGGAAACTA- :::::: CTGGGAGCAAG
1440 1450 1460 AGCTGTTGTTCATGAAATTGTGAG- :::::::::::::::::::::::::::::::::::	1510 GAACAATTTTC ::: :: : GAAGCATCATC	1570 TGGGCAGAGGAGAA ::: ::: :: TGGCTGGAGGGGTA	1630 rcarcraraga : :: : rgcrccagrco
			1620 TGC-TGAC' :: :: -GCTTGGA
pmsgen CHKTFE	DWSGEN CHKTFE	pmsgen CHKTFE	pmsgen CHKTFE
	SUDSTITUTE STILET	(1.022 20)	

				27	48				
1730	TTGAAGGC	••	CAGAGAGC	1680	1790	GCATGCCC		GGCCTGGA	
1720	SATGAAGGCT	•••	SCAGCAGTCT	1670	1780	SAGTTCAGTG		GTTCCTCTT	1720 1730
1710	SAAAAGCCCTC	••	SAAGAATCCAC	1660	1770	CCTTCCCCAC		AAAAGCAGTI	1720
1700	CAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGC		TGAAGGGGGGT	1650	1760	CTAAAAAAAGT	••	CAGACTGGGT	1710
1690	CACAACCTAA	••	GGGAGTATTA	1640	1750	SAAAGTTGGAC	•••	CAGACTTGGCC	1700
1680	pmsgen TACAGCTTGGTACA	•••	CHKTFE TATATGCTGCTGGGGAGTATTATGAAGGGGGTGAAGAATCCAGCAGCAGTCTCAGAGAGC	1630	1740	pmsgen AAATCTCTTTATGAAAGTTGGACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCC	••	CTCTATAACAGACTTGGCCCAGACTGGGTAAAAGCAGTTGTTCCTCTTGGCCTGGA	1690
	pmsgen		CHKTFE	UTE S		pmsgen		CHKTFE	
	S	UBS	STIT	UTE S	HEE	r (R	ULE	26)

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31	-TT	ITC	ACT
164	: :	'AGA'	\TG-
164 164 311	0 1240 1250 CAAAGTGCCCTACAATGTTGGACCTGGCTT	GTTGGAATAT 660	1310 ACTCT-ACCAA' :::::::: ACTGTGAACAA'
' end.	1240 rgccctacaa	GTCCTCCTA 650	1300 SCACATC-CA : : :: STGAAGCTCA 710
in receptor mRNA, 3' end nt overlap	1210 1230 1240 1250 pmsgen ccaccagaragcrggaggaggaggrgcrgaaagrgcccracaargrrggaccrggcrr-	AAAAACATGGAAGGAAACTGTCCTCCTAGTTGGAATATAGATTC 630 640 650	1260 1270 1280 1290 1300 1310 pmsgen -TACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATC-CACTCT-ACCAATG RATTRF CTCATGTAAGCTGGAACTTTCACAGAATCAAAATGTGAAGCTCGTGAACAATGTACT 670 680 690 700 710
	1220 CTGGAGAGGA	TCAAAAACAT 630	1280 TCTACACAAA :: : SAACTTTCACA
TTKFR Rat transferri 55.5% identity in 560	1210 CCAGATAGCAG	RATTRF TGCAGAAAAGCTATTC1 610 620	1260 1270 pmsgen -TACTGGAAACTTTTC : :: :: RATTRF CTCATGTAAGCTGGAA
RATTRFR 55.5% id		RATTRF TGC	
	55551110	TE OTILL!	(

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1370 CAGACAG :::::	1430 CTCAGAG :::: TCCAGTG	1480 -AAAAGGAA ::: :: TCAAAAGAT 00	40 TGGTCTT :::: TGGAGCT
1360 AGTGGAACCAGACAG : ::::::::: FGAGGAACCAGACCG	1420 FATTGACC: ::	14 CTGAA ::: ATGATTTC 900	1540 SAAGAATTTG ::::::::: SGAGACTATG 960
1350 CAGAGGAGC : ::: TAAAGGCTA	390 1400 1410 1420 GTCACCGGGACTCATGGGTGTTTGGTGTATTGA :: ::: ::: ::: ::: ::: ::: ::: ::: :::	1470 TTTGGAACA-(:: : : ATTCTCAGAT2 890	1510 1520 1530 1540 GAACAATTTTGTTTGCAGGATGCAGAAGAATTTTGGTCTT : :::::::::::::::::::::::::::::::::
1350 TACTCTCAGAGG : : : :: CGTTATTAAAGG	14 ATGGGTG1 :::: TTGGGGCC	0 GGAGCTTT :: :: CAAGTATT	1520 GCAAGCTG :::::: GCCAGCTG
1340 STGATAGGT, : :: ATCTTTGGC	1400 CGGGACTCA' : :: : AGAGACGCT' 820	150 1460 ATGAAATTGTGAG ::::: FTGAAACTTGCCC 870 8	1510 ATTTTGTTT ::::::: ATTATCTTT 30
1330 TTACAATO :: ACTTAACO	1390 AGGTCAC(:: :: AGCCCAG	1450 TTCATGAA : ::: CTGTTGAA 870	15 AGAACAAT" :: :: AGGAGTAT"
1320 1330 1340 1350 1360 1370 pmsgenAAGTGACAGTTTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAGACAG :::::::::::::::::::::::::::	1380 1390 1400 1410 1420 1430 pmsgen ATATGTCATTGGGGGGTCTCATGGGTGTTTGGTGGTATTGACCCTCAGAG ::::::::::::::::::::::::::::::::::	1440 1450 1460 1470 1480 pmsgen T-GGAGCTGTTCATGAAATTGTGAGGAGCTTTGGAACA-CTGAAAAAGGAA :::::::::::::::::::::::::::	1490 1510 1520 1530 1540 GGGTGGAGACCTAGAACTTTTGTTTTGCAAGCTGGGATGCAGAATTTTGGTCTT : : : : : : : : : : : : : : : : : : :
1 nAAGTG ::: F GAAAGAA	n ATATGTC::::	144 T-GGAGCAGC ::::::	
pmsgen RATTRF		(95 BYTTRF	pmsgen RATTRF
		(11022 20)	

					30	0/4	8							
1600	GTGGCGTG	••	GCTTTC	1020	1660	GATTGTAC	••	TCTGCCAG	1080	1720	TGATGAAG	••	CGA	
1590	CTTCAAGAG	•••	CATCTAAAG-	0	1650	PCTGAGAGT	•••	TTCAAGGTT	1070	1710	AAAAGC-CC	••	TAAAGCATC	1130
1580	<i>PTCAAGACTC</i>	••	FTCATCTTTG	1010	1640	AAACTA-CAC	••	TACTAGCAAG	1060	1700	AAAAGAGCTG	••	GCAGGACG	1120
1570	SAGGAGAA	×	SAGGGGTACCT	990 1000	1630	CTATAGAAGGA	••	GTCGTCCTGG	1050	1690	CTTGGTACACCTAACAAAAGAGCTGAAAAGC-CCTGATGAAG	•••	GGGAAGATAAT	1110
1560	TGAGTGGGCA	••	TGAGTGGCTGG	56 086	1620	TGCTGACTCAT	••	F-CTGGATAAA	1040	1680	CAGCTTGGTA	••	TACACTTATG	1100
1550	CTTGGTTCTACTGAGTGGGCAGAGAGATTCAAGACTCCTTCAAGAGCGTGGCGTG	•••	RATTRF GTTGGTCCGACTGAGTGGCTGGAGGGGTACCTTTCATCTTTGCATCTAAAGGCTTTC	970 9	1610	pmsgen GCTTATATTATGCTGACTCATCTATAGAAGGAAACTA-CACTCTGAGAGTTGATTGTAC	••	RATTRF ACTTACATTAAT-CTGGATAAAGTCGTCCTGGGTACTAGCAACTTCAAGGTTTCTGCCAG	1030	1670	pmsgen ACCGCTGATGTACAG	•••	RATTRF CCCCCTATTATACACTTATGGGGAAGATAATGCAGGACGTAAAGCATCCGA-	1090
	o bmsgen	JBS		JTË SI	HEE"		JLE) .		pmsgen		RATTRF (

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CTTTGAAGGCAAATCTCTTTAT-GAAAGTTGGACTAAAAAAAGTCCTTCCCCAG :::::::::::::::::::::::::::::::::	CCAGGATAAGCAAATTGGGATCTGGAAATGATTTTGAGGTGTTCT	CATTCCCTTTTCTTGCATATTCAGGAATCCCAGCAGTTTCTTTC
50 1760 TTGGACTAAAAAAGT ::::::::::::::::::::::::::::::	1820 GGAAATGATTT	GGAATCCCAGC 1240
1750 AGTTGG : ::: CAGTAATTGG	1810 ATTGGGATCT	rgcatatrca 1230
T740 CTCTTTAT-GAA:::::::::::::::::::::::::::::	1800 3GATAAGCAAJ	rcccrttrcr 1220
TTGAAGGCAAATCTCTT:::::::::::::::::::::::	1150 1790 GCATGCCCAO	ATGCTGCATI 1210
pmsgen GCTTTGAAGGCAAAT	1140 1780 pmsgen AGTTCAGTGGCATGC	RATTRF CCTTGGACAATGCTG(
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FIGURE 16-9

Human transferrin receptor mRNA, complete cd identity in 464 nt overlap 54.3% HUMTFRR

HUMTFR TATGGAAGGAGACTGTCCCTCTGACTGGAAAACAGACTCTACATGTAGGATGGTAACCTC pmsgen AGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTAC-TGGAAACTTTTCTACAC

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pmsgen ccgccactcatcgtgtttcgtcgtattcacctcacact-ccacactcttcatc ••

HUMTFR GAGAGGTGCATGGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA

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		•	
1460 1470 1480 1490 1500 pmsgen AAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAACAA ::::::::::::::::::::::::::::::::	1520	1570 1580 1590 1600 1610 1620 A-GGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCT : :: : : : : : : : : : : : : : : : :	1630 1640 1650 1660 1670 1680 pmsgen ATAGAAGCTACACTCTGAGGTTGATTGTACACCGCTGATGTACA-GCTTGGT-AC : :::::::::::::::::::::::::::::::::::
1480 1490 AAAAAGGAAGGGTGG ::: X::: TTAAAAGATGGGTTT	1550 TCTTCTTGGT ::::: ATCGGTTGGT	1610 TGGCTTATATTAATGC : ::::X TCACTTATATTAATCT	1670 CACCGCTGATC :: :: :: 3CCCACTGTTC
1480 ACACTGAAAAA : : :: ATGGTCTTAAA	1530 1540 TGCAGAAGAATTTGGT ::::::::: TGCTGGAGACTTTGGA	1600 GAGCGTGGCG' : TTAAAGGCTT'	1660 GTTGATTGTA ::: :: : GTTTCTGCCA(
1470 SAGCTTTGGAA : :: : STTCTCAGATA	1530 TGGGATGCAG ::: ::::	1590 ACTCCTTCAA : :: :: TC-CCTGCAT	1650 CACTCTGAGAGTTG :: ::: CAACTTCAAGGTTT
1460 TTGTGAG ::: :: TTGCCCAGAT	1510 1520 TTTTGTTTGCAAGC :::::::::: TTATCTTTGCCAGT 1440 1450	1570 1580 pmsgen A-GGAGAATTCAAG : :: : : : : : : : : : : : : : : : : :	1630 1640 ATAGAAGGAAACTA : : : : : : : : : : : : : : : : : : :
pmsgen AAATTG-:::::HUMTFR AACTTGC	1510 pmsgen TTT' :: HUMTFR TTA'	1570 pmsgen A-GG ::: HUMTFR AGGG	1630 pmsgen ATAG : HUMTFR GTTC
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1740	ACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATG		HUMTFR AAAACAATGCAAAATGTGAAGCATCCGGTTACTGGGCAATTTCTATATCAGGACAGCAAC	1670
1730	TTTGAAGGCA		ATTTCTATA	1660
1720	TGATGAAGGC		TTACTGGGCA	1650
1710	FGAAAAGCCC		AAGCATCCGG	1640
1700	ACAAAAGAGC	••	SCAAAATGTG	1630
1690		••	AAAACAATC	1620
	pmsgen		HUMTFR	

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FIGURE 17B

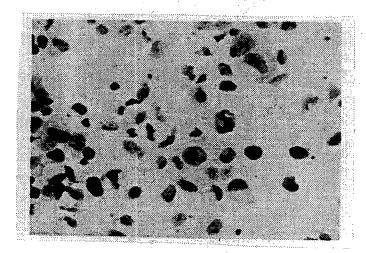
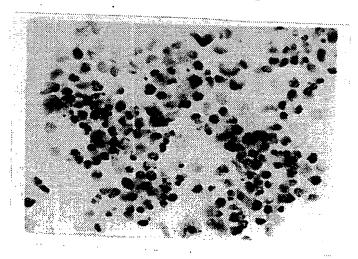


FIGURE 17C



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FIGURE 18

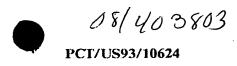
1 2 100 -68 -43 - WO 94/09820

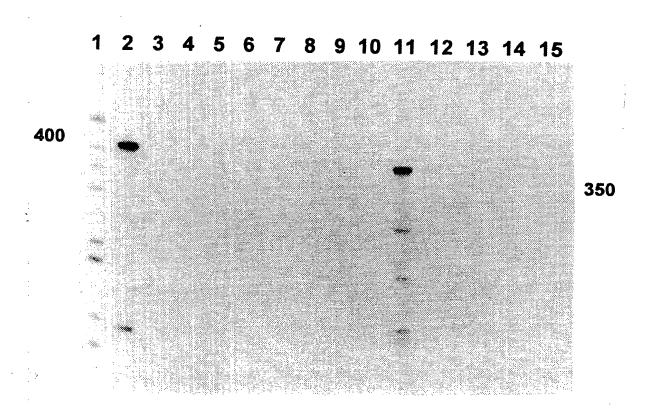
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FIGURE 19

1 2 3 4

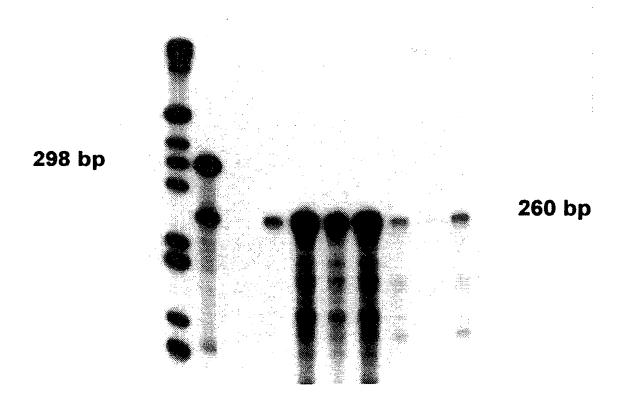
200 kDa — PSM
69 kDa —



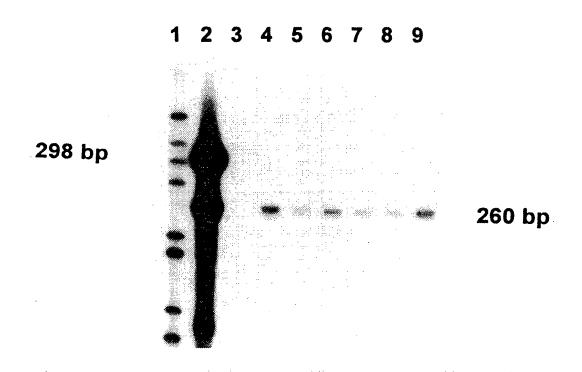


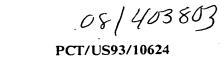
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1 2 3 4 5 6 7 8 9 10



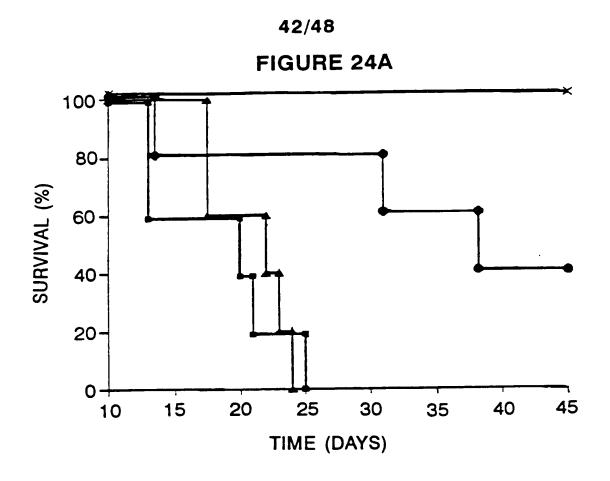
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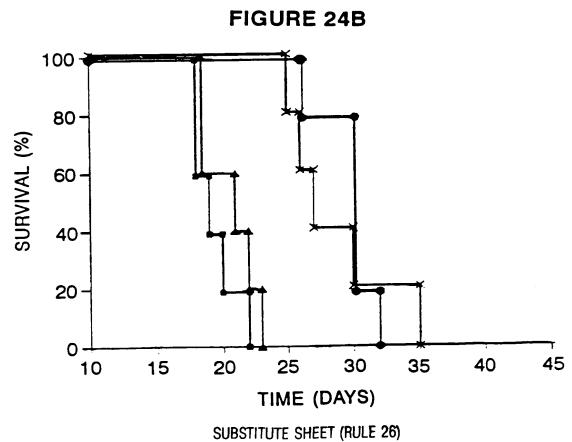


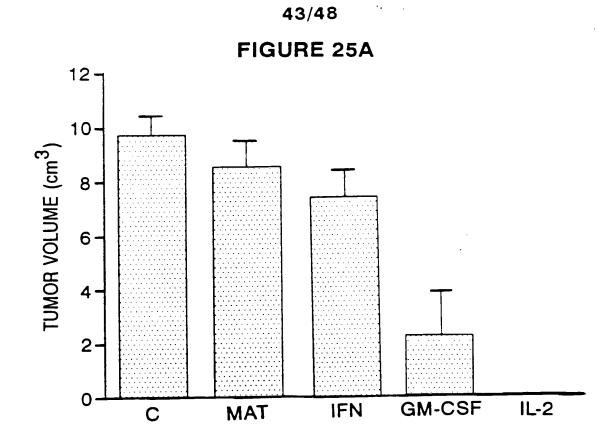


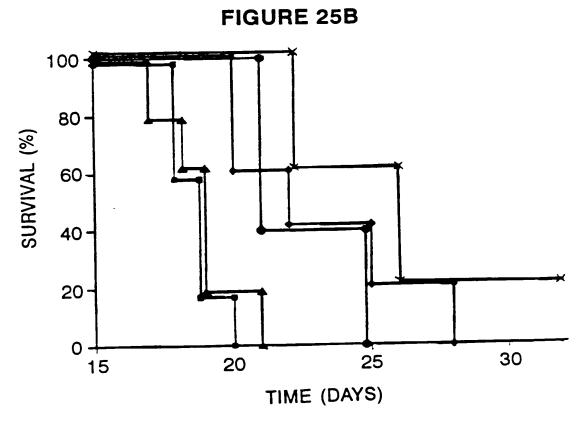
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CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	_	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	_
R1564 (RAT MAMMARY)	NO	YES	_	-
R1564-11-c14	YES	YES	_	+
R1564-11-c15	YES	YES	_	REPEAT
R1564-11-c16	YES	YES	_	ND
R1564-11-c12	YES	YES	ND	+
		<u> </u>		<u> </u>



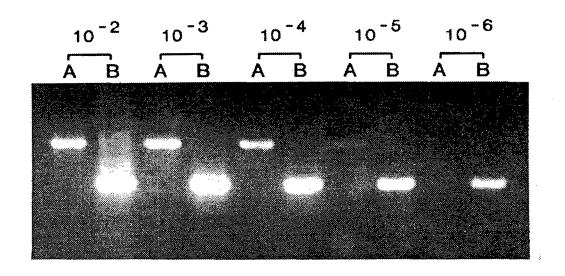


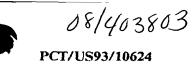


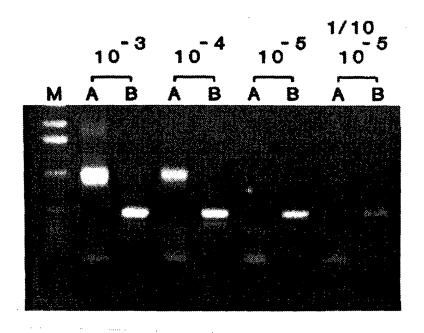


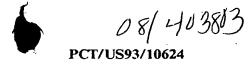
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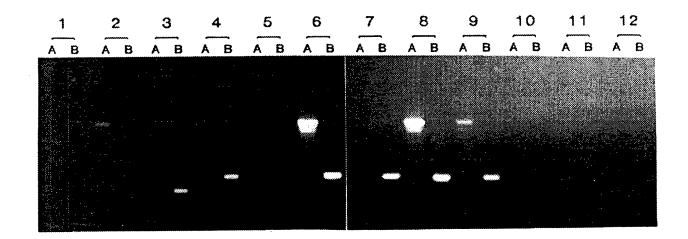
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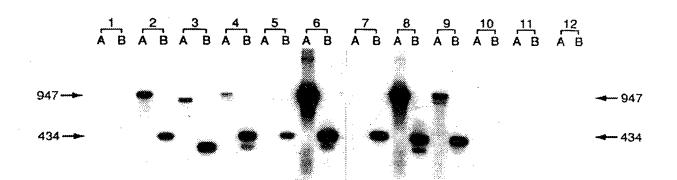


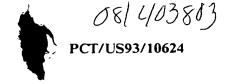




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		1100112				
Patient	Stage	Tr_atment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	_	+
2	T2NoMo	RRP 7/93	6.1	_	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	_	+
4	T2BNoMo	RRP 3/92	NMA	0.4	_	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	_	+
6	Recur T3	I-125 1986	54.7	1.4	_	+
7	ТЗАМоМо	RRP 10/92	NMA	0.3	_	+
8	ТЗNхМо	XRT 1987	7.5	0.1	-	_
9	T3NxMo	Proscar + Flutamide	35.4	0.7	_	-
10	D2	S/P XRT Flutamide +Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	_	+
13	ТЗМоМо	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	- (
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-

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